

BLASTP 2.2.20+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: YSX40DNX016

Database: Protein sequences derived from the Patent division of GenBank

644,914 sequences; 121,161,582 total letters

Query=Length=16

Sequences producing significant alignments:	Score (Bits)	E Value
gb AAA02142.1  Sequence 1 from Patent US 4885357	20.2	0.45
gb AAA55740.1  Sequence 14 from Patent EP 0330191	18.9	1.1
gb AAA53711.1  Sequence 3 from Patent WO 9000563	18.9	1.1
gb AAA56309.1  Sequence 7 from Patent EP 0196864	18.0	2.0
gb AAA54420.1  Sequence 14 from Patent WO 8806628 >gb AAA5600...	18.0	2.0
gb AAA54815.1  Sequence 19 from Patent WO 8607383	17.6	2.6
gb AAA53695.1  Sequence 2 from Patent WO 9004640	17.2	3.5
gb AAA54560.1  Sequence 2 from Patent WO 8805081 >gb AAA56055...	16.8	4.7
gb AAA54001.1  Sequence 2 from Patent WO 8906283 >gb AAA54156...	15.9	8.5
gb AAA00924.1  Sequence 1 from Patent US 4657891	15.9	8.5

## ALIGNMENTS

>gb|AAA02142.1| Sequence 1 from Patent US 4885357  
Length=21

Score = 20.2 bits (40), Expect = 0.45  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 10 LLALLA 15  
          LLALLA  
Sbjct  8   LLALLA 13

Score = 16.3 bits (31), Expect = 6.4  
Identities = 7/11 (63%), Positives = 7/11 (63%), Gaps = 2/11 (18%)

Query  5   LLPAVLLALLA 15  
          LL    LLAL A  
Sbjct  8   LLA--LLALFA 16

>gb|AAA55740.1| Sequence 14 from Patent EP 0330191  
Length=27

Score = 18.9 bits (37), Expect = 1.1  
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query  5   LLPAVLLAL 13  
          LLP +LLAL

Sbjct 9 LLP-LLLAL 16

Score = 15.1 bits (28), Expect = 15  
Identities = 6/10 (60%), Positives = 6/10 (60%), Gaps = 3/10 (30%)

Query 5 LLPAVLLALL 14  
      LL LL LL  
Sbjct 7 LL---LLPLL 13

>gb|AAA53711.1| Sequence 3 from Patent WO 9000563  
Length=99

Score = 18.9 bits (37), Expect = 1.1  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 2 AVALLPA 8  
      AVALL A  
Sbjct 6 AVALLAA 12

Score = 15.1 bits (28), Expect = 15  
Identities = 6/8 (75%), Positives = 6/8 (75%), Gaps = 2/8 (25%)

Query 8 AVLLALLA 15  
      AV ALLA  
Sbjct 6 AV--ALLA 11

>gb|AAA56309.1| Sequence 7 from Patent EP 0196864  
Length=77

Score = 18.0 bits (35), Expect = 2.0  
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 2/10 (20%)

Query 2 AVALLPAVLL 11  
      A+ALLP LL  
Sbjct 7 ALALLP--LL 14

Score = 14.6 bits (27), Expect = 21  
Identities = 4/4 (100%), Positives = 4/4 (100%), Gaps = 0/4 (0%)

Query 11 LALL 14  
      LALL  
Sbjct 8 LALL 11

Score = 9.1 bits (14), Expect = 943  
Identities = 2/2 (100%), Positives = 2/2 (100%), Gaps = 0/2 (0%)

Query 13 LL 14  
      LL  
Sbjct 69 LL 70

>gb|AAA54420.1| Sequence 14 from Patent WO 8806628  
gb|AAA56005.1| Sequence 5 from Patent EP 0281363  
Length=91

Score = 18.0 bits (35), Expect = 2.0  
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 2/10 (20%)

Query 2 AVALLPAVLL 11  
A+ALP LL  
Sbjct 7 ALALLP--LL 14

Score = 14.6 bits (27), Expect = 21  
Identities = 4/4 (100%), Positives = 4/4 (100%), Gaps = 0/4 (0%)

Query 11 LALL 14  
LALL  
Sbjct 8 LALL 11

>gb|AAA54815.1| Sequence 19 from Patent WO 8607383  
Length=22

Score = 17.6 bits (34), Expect = 2.6  
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 2/12 (16%)

Query 3 VALLPAVLLALL 14  
+AL A+LL LL  
Sbjct 6 IAL--ALLPLLL 15

Score = 15.5 bits (29), Expect = 11  
Identities = 5/6 (83%), Positives = 5/6 (83%), Gaps = 0/6 (0%)

Query 11 LALLAP 16  
LALL P  
Sbjct 8 LALLLP 13

>gb|AAA53695.1| Sequence 2 from Patent WO 9004640  
Length=86

Score = 17.2 bits (33), Expect = 3.5  
Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 7 PAVLLALL 14  
PAV+L LL  
Sbjct 3 PAVILFLL 10

>gb|AAA54560.1| Sequence 2 from Patent WO 8805081  
>gb|AAA56055.1| Sequence 11 from Patent EP 0273774  
Length=24

Score = 16.8 bits (32), Expect = 4.7  
Identities = 8/13 (61%), Positives = 8/13 (61%), Gaps = 3/13 (23%)

Query 4 ALLPAVLLALLAP 16  
ALL LL LL P  
Sbjct 8 ALL---LLLLLP 17

Score = 15.9 bits (30), Expect = 8.5

Identities = 7/11 (63%), Positives = 8/11 (72%), Gaps = 2/11 (18%)

Query 4 ALLPAVLLALL 14  
       AL A+ LALL  
 Sbjct 2 AL--AITLALL 10

Score = 15.5 bits (29), Expect = 11  
 Identities = 7/13 (53%), Positives = 9/13 (69%), Gaps = 2/13 (15%)

Query 2 AVALLPAVLLALL 14  
       A+ L A+LL LL  
 Sbjct 4 AITL--ALLLLL 14

>gb|AAA54001.1| Sequence 2 from Patent WO 8906283  
 gb|AAA54156.1| Sequence 42 from Patent WO 8900999  
 Length=30

Score = 15.9 bits (30), Expect = 8.5  
 Identities = 7/12 (58%), Positives = 7/12 (58%), Gaps = 3/12 (25%)

Query 1 AAVALLPNAVLLA 12  
       AA LL LLA  
 Sbjct 8 AAAGLL---LLA 16

Score = 12.9 bits (23), Expect = 67  
 Identities = 7/13 (53%), Positives = 7/13 (53%), Gaps = 2/13 (15%)

Query 5 LLPAVL--LALLA 15  
       LLP L LLA  
 Sbjct 4 LLPTAAAGLLLLA 16

>gb|AAA00924.1| Sequence 1 from Patent US 4657891  
 Length=48

Score = 15.9 bits (30), Expect = 8.5  
 Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 0/12 (0%)

Query 4 ALLPAVLLALLA 15  
       ALL + L ALLA  
 Sbjct 6 ALLKSCLRALLA 17

Database: Protein sequences derived from the Patent division of GenBank  
 Posted date: Apr 17, 2009 6:11 PM  
 Number of letters in database: 54,892  
 Number of sequences in database: 1,417

Lambda K H  
 0.335 0.297 1.50

Gapped

Lambda K H  
 0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1  
 Number of Sequences: 1417

Number of Hits to DB: 0  
Number of extensions: 0  
Number of successful extensions: 0  
Number of sequences better than 200000: 0  
Number of HSP's better than 200000 without gapping: 0  
Number of HSP's gapped: 0  
Number of HSP's successfully gapped: 0  
Length of query: 16  
Length of database: 54892  
Length adjustment: 5  
Effective length of query: 11  
Effective length of database: 47807  
Effective search space: 525877  
Effective search space used: 525877  
T: 11  
A: 40  
X1: 1 (0.5 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 1 (3.6 bits)  
S2: 0 (3.2 bits)